SEQUENCE LISTING

<110> Kato, Sei
Kimura, Tomoko
Ohkine, Shinji
Kobayashi, Midori

<120> HUMAN PROTEINS HAVING TRANSMEMBRANE DOMAINS AND DNAs ENCODING THESE PROTEINS

<130> GIN-6711PUS

<150> JP 9/276271
<151> 1997-10--

<140> 09/529,205
<141> 2000-0?-21

<160> 49

<170> PatentIn Ver. 2.0

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Leu Lys Lys Asp Gly Asn Asp Lys Leu Cys Trp Val Ser Ala Arg Glu
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gccgacgtga aggagtgcgc cgccgggcac ctgtaccgca tcaacgtgtg catgaagcac 120
tgccgcctgg cctgcctgtg ccgcgagcgc gtctacgacc cgcgcatgtg gaagaaggcc 180
[illegible] 240
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[illegible] 360
[illegible] 420
[illegible] 480
[illegible] 534

[illegible]

<210> 20
<211> 390
<212> DNA
<213> Homo sapiens

<400> 20
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cagaagcgcc tgcaggagtg ccctgaagcg ctggctgtgg tcgggatcgg ctcgcagttc 120

ttcaatgttc tcgtcaattt ggtcctgctg gccaacctgc tctggttcta caaggcgagg 180

gctgaggcag agcaggagct cagcttcaga ctgggagtcc tcagcctcgc cgtcaccgtg 240

gaagcagaga tagcgctgtt cgtcgtgtcc ctgctcgacg tgtgcttcgt gtgcctcctg 300

[illegible]

[illegible]

<210> 21
<211> 474
<212> DNA
<213> Homo sapiens

[illegible]

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 1               5                  10

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Leu Val Leu Ser Ser Phe Ala Gly Tyr Ala Arg Ser Thr Ser Cys Glu Val
            15                  20                  25

caa gtt agc aac gac gtt tgc cag gtg aac gaa tgc gac gac aac acc gac      96
Gln Val Ser Asn Asp Val Cys Gln Val Asn Glu Cys Asp Asp Asn Thr Asp
        30                  35                  40

ggg tct cag tgt tgg aac gct cgt atc cgt gcg gtt ggt ctg ctg acc gtt     144
Gly Ser Gln Cys Trp Asn Ala Arg Ile Arg Ala Val Gly Leu Leu Thr Val
    45                  50                  55                  60

atc tct aag ggt tgc tct ctg aac tgc gtt gac gac tct cag gac tac tac     192
Ile Ser Lys Gly Cys Ser Leu Asn Cys Val Asp Asp Ser Gln Asp Tyr Tyr
                65                  70                  75

gtt ggt aag aac atc acc tgc tgc gac act gac ctg tgc aac ggt gct tct     240
Val Gly Lys Asn Ile Thr Cys Cys Asp Thr Asp Leu Cys Asn Gly Ala Ser
            80                  85                  90

ggt gct cac gct ctg cag ccg gct gct gct atc ctg gct ctg ctg ccg gct     288
Gly Ala His Ala Leu Gln Pro Ala Ala Ala Ile Leu Ala Leu Leu Pro Ala
        95                 100                 105

ctg ctg ctg gct ctg ggt ccg ggt cag ctg                                 312
Leu Leu Leu Ala Leu Gly Pro Gly Gln Leu
    110                 115                 120

taggctttgg gggtttccgc tgcaggtcac actgtttgtg gtgcccgagg cctctgtgtg      372

actcctcaca gttttggccc agttgggtac gcctatggtt ctgaggtcac attttcacag      432

aagtctgtcc atgttgtgtt ggaccctgct cctcgacctt gacctctcca tgcctctcag      492

caggattccc attttgcaga tcagctttag tgttccagat tcgcctgtag atgtttctct      552

caacctctc tgttgctgtt tccatgggcc agtcattcct gcctctgtcg ctgtttgtcg      612

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa                                     644
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<4> ...
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1 5 10 15

Pro Gly Thr Ala Leu Leu Cys Tyr Ser Cys Lys Ala Gln Val Ser Asn
20 25 30

Glu Asp Cys Leu Gln Val Glu Asn Cys Thr Gln Leu Gly Glu Gln Cys
35 40 45

Trp Thr Ala Arg Ile Arg Ala Val Gly Leu Leu Thr Val Ile Ser Lys
50 55 60

Gly Cys Ser Leu Asn Cys Val Asp Asp Ser Gln Asp Tyr Tyr Val Gly
65 70 75 80

Lys Lys Asn Ile Thr Cys Cys Asp Thr Asp Leu Cys Asn Ala Ser Gly
85 90 95

Ala His Ala Leu Gln Pro Ala Ala Ala Ile Leu Ala Leu Leu Pro Ala
100 105 110

Leu Gly Leu Leu Leu Trp Gly Pro Gly Gln Leu
115 120

<210> 23
<211> 1079
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (205)..(567)

<400> 23
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cgccgagagc gtcgggcgcc ccgccgtcag ccgcgcgccg cggtcagccg ccgccgccgc 120

[illegible] 180

[illegible] 240

[illegible] 300

[illegible] 360
Gly Leu Glu Ile Thr Gly Thr Ala Leu Ala Val Leu Gly Trp Leu Gly
1 5 10 15

[illegible] 420
Thr Ile Val Tyr Tyr Ala Leu Ile Met Trp Ala Val Ala Ala Ile

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aac tgc gtc gtg cag tcg acc ggg cag atg ggc cag tgc aag gtg tac gac      432
Asn Cys Val Val Gln Ser Thr Gly Gln Met Gly Gln Cys Lys Val Tyr Asp
                50                  55                  60

tcc ctg cag gcg gcc ctc aag gac cgc ctg cag gcc agc cgc gcc agc ctc      480
Ser Leu Gln Ala Ala Leu Lys Asp Arg Leu Gln Ala Ala Arg Ala Ser Leu
            65                  70                  75                  80

gtc gtg gcc atc atc ttc ctg gcc gtc ctc gac tcc gtc gtg ggc gtg tcc      528
Val Val Ala Ile Ile Leu Leu Ala Val Phe Gly Leu Leu Val Ala Leu Val
                85                  90                  95

ggc gcc cag tgc acc aac tgc gtg cag gac gac acc gcc aag gcc aag      576
Gly Ala Gln Cys Thr Asn Cys Val Gln Asp Asp Thr Ala Lys Ala Lys
            100                 105                 110

atc acc atc gtg gcc gtc ggc gtg ctc ttc ctc ctg gcc gcc ctc ctc acc      624
Ile Thr Ile Val Ala Val Gly Val Leu Phe Leu Leu Ala Ala Leu Leu Thr
        115                 120                 125

ctc gtg ccg gtg tcc tgg tcc gcc aac acc atc cgg gac ttc tac      672
Leu Val Pro Val Ser Trp Ser Ala Asn Thr Ile Ile Arg Asp Phe Tyr
    130                 135                 140

aac ccc gtg gtg ccc gag gcg cag aag cgc gag atg ggc gcg ggc ctg      720
Asn Pro Val Val Pro Glu Ala Gln Lys Arg Glu Met Gly Ala Gly Leu
145                 150                 155                 160

tac gtg ggc tgg gcg gcc gcg gcg ctg cag ctg ctg ggg ggc gcg ctg      768
Tyr Val Gly Trp Ala Ala Ala Ala Leu Gln Leu Leu Gly Gly Ala Leu
                165                 170                 175

ctc tgc tcc tgc ccc ccg cgc gag aag aag tac acg gcc acc aag      816
Leu Cys Cys Ser Cys Pro Pro Arg Glu Lys Lys Tyr Thr Ala Thr Lys
            180                 185                 190

gtc gtc tac tcc gcg ccg agc acg ggc ccg ggc gcc tcc ctg ggc      864
Val Val Tyr Ser Ala Pro Arg Ser Thr Gly Pro Gly Ala Ser Leu Gly
        195                 200                 205

tcc ggc tac agg aac gac tac gtc                                  894
Ser Gly Tyr Arg Asn Asp Tyr Val
    210                 215
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<400> 24
<211> 168
<212> PRT
<213> Homo sapiens

<400> 24
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1 5 10 15

Trp Leu Gly Thr Ile Val Cys Cys Ala Leu Ile Met Trp Arg Val Ser
20 25 30

Ala Phe Ile Gly Ser Asn Ile Ile Thr Ser Gln Asn Ile Trp Glu Gly
35 40 45

Leu Trp Met Asn Cys Val Val Gln Ser Thr Gly Gln Met Gln Cys Lys
50 55 60

Val Tyr Asp Ser Leu Leu Ala Leu Pro Gln Asp Leu Gln Ala Ala Arg
65 70 75 80

Ala Leu Ile Val Val Ala Ile Leu Leu Ala Ala Phe Gly Leu Leu Val
85 90 95

Ala Leu Val Gly Ala Gln Cys Thr Asn Cys Val Gln Asp Asp Thr Ala
100 105 110

Lys Ala Lys Ile Thr Ile Val Ala Gly Val Leu Phe Leu Leu Ala Ala
115 120 125

Leu Leu Thr Leu Val Pro Val Ser Trp Ser Ala Asn Thr Ile Ile Arg
130 135 140

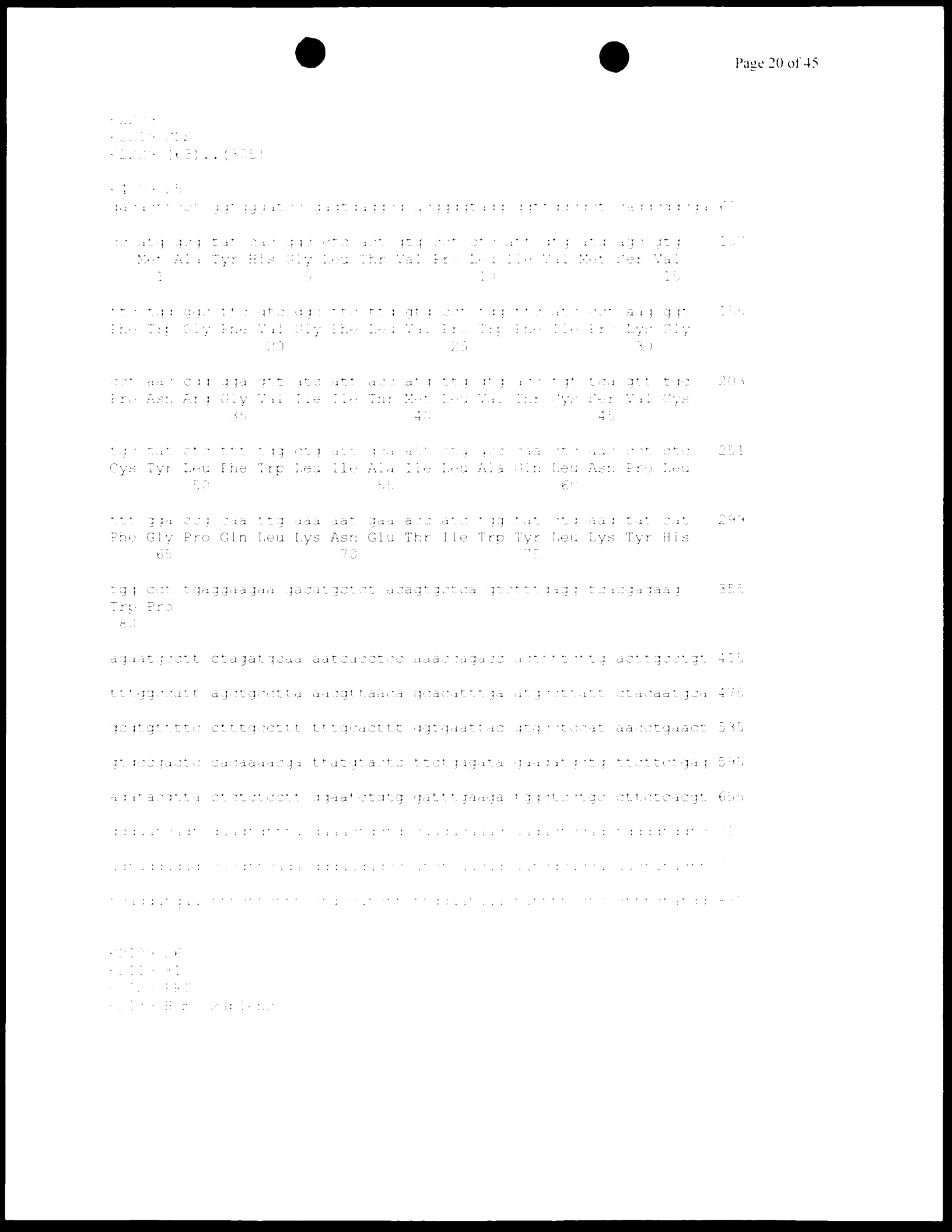
Asp Phe Tyr Asn Pro Val Val Pro Glu Ala Gln Lys Arg Glu Met Gly
145 150 155 160

Ala Gly Leu Tyr Val Gly Trp Ala Ala Ala Ala Leu Gln Leu Leu Gly
165 170 175

Gly Ala Leu Leu Cys Cys Ser Cys Pro Arg Lys Thr Thr Asn Tyr Gly
180 185 190

Ala Thr Lys Gly Leu Thr Trp Ser Ala Ser Val Met Ala Leu Leu Ala
195 200 205

Ser Leu Gly Thr Gly Tyr Ala Leu Met Lys Tyr Val Gly Ile Val Ala
210 215 220



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Trp Gly Phe Val Gly Phe Leu Val Pro Trp Phe Ile Ser Lys Gly Pro
            20                  25                  30

Asn Asn Gly Val Ile Ile Thr Met Leu Val Thr Cys Ser Val Cys Lys
        35                  40                  45

Tyr Leu Phe Trp Leu Ile Ala Ile Leu Ala Gln Leu Asn Ser Leu Phe
    50                  55                  60

Gly Pro Gln Leu Lys Asn Glu Thr Ile Trp Tyr Leu Lys Tyr His Trp
65                  70                  75                  80

Pro

<210> 27
<211> 1127
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (128)..(1027)

<400> 27
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ctgtccagtg tcccaggctg ctgagctctc gccgccgag acctcgtggc gaggcgcag 120

ggc atg cta gcc ttg cgc gtg gcg cgc ggc tcg tgg ggt gcc ctg agg      169
     Met Leu Ala Leu Arg Val Ala Arg Gly Ser Trp Gly Ala Leu Arg
       1               5                  10                  15

ggc gcc gct tgg gct ccg ggg acg cgg ccg agt aag cga cgc gcc tgc      217
Gly Ala Ala Trp Ala Pro Gly Thr Arg Pro Ser Lys Arg Arg Ala Cys
                   20                  25                  30

tgg gcc ctg ctg ccg ccg gtg ccg tgc tgc ctg ggc tgc ctg gcc gaa      265
Trp Ala Leu Leu Pro Pro Val Pro Cys Cys Leu Gly Cys Leu Ala Glu
               35                  40                  45

                                                                    313
Arg Trp Arg Leu Arg Arg Ala Ala Leu Gly Leu Arg Leu Arg Gly Leu
           50                  55                  60

                                                                    361
Gly Gln Arg Asn His Cys Ser Gly Ala Gly Lys Ala Ala Ile Arg Pro
       65                  70                  75

                                                                    409
Ala Ala Gly Ala Lys Arg Ala Ala Ala Pro Arg Ile Lys Gly Gly Thr Trp Lys
   80                  85                  90                  95
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atg ttg tta atg aca aca act att ttt tct tca ttt ttg ttt tat tta      [illegible]
Met Leu Leu Met Thr Arg Ile Gly Leu Ala Pro Val Leu Gly Tyr Leu
                110                 120                 125

att att gaa tta tat ttt gat att gta tta gga gtt ttt gtt ttt gta gat   960
Ile Ile Glu Leu Asp Phe Asn Ile Val Leu Gly Val Phe Ala Leu Ala
            130                 135                 140

gga tta ata tat ttg ttt tat gtt tta ttt att ttt gca aac ttg ttt gca   912
Gly Leu Ile Asp Leu Leu Asp Gly Phe Ile Ala Arg Asn Trp Ala Asn
        145                 150                 155

caa aga tta act ttg gta gat gtt gtt tat tca gtt gtt tat ata aaa ata   960
Gln Arg Leu Thr Leu Gly Ser Ala Leu Asp Pro Leu Ala Asp Lys Ile
    160                 165                 170                 175

ctt atc agt atc tta tat gtt agt tta act tca gat gtt tat ata aca      912
Leu Ile Ser Ile Leu Tyr Val Ser Leu Thr Tyr Ala Asp Leu Ile Pro
                180                 185                 190

gtt cca ctt act tac atg ata att tcg aga gat gta atg tta att gct      960
Val Pro Leu Thr Tyr Met Ile Ile Ser Arg Asp Val Met Leu Ile Ala
            195                 200                 205

gct gtt ttt tat gtc gta aga tac gga act ctt cca aca gca gga aga ctt   912
Ala Val Phe Tyr Val Arg Tyr Gly Thr Leu Pro Thr Ala Gly Arg Leu
        210                 215                 220

gcc aag tat ttc aat cct tgt tat gcg act gct agg tta aaa cca aga ata   960
Ala Lys Tyr Phe Asn Pro Cys Tyr Ala Thr Ala Arg Leu Lys Pro Thr
    225                 230                 235

ttc atc agc aag gtg aat aca gca gtc cag tta atc ttg gtg gta gca gtt   912
Phe Ile Ser Lys Val Asn Thr Ala Val Gln Leu Ile Leu Val Ala Ala
240                 245                 250                 255

tct ttg gta gtt gtt cca gtt ttt aat tat gtt gac agc atc tat tta tta   960
Ser Leu Ala Ala Pro Val Phe Asn Tyr Ala Asp Ser Ile Tyr Leu Leu
                260                 265                 270

[illegible]                                                          [illegible]

tat tat cat tat ggg aga aaa act gtt caa gtt ata aag                  [illegible]
Tyr Tyr His Tyr Gly Arg Lys Thr Val Gln Val Ile Lys Arg
            275                 280

[illegible]                                                          [illegible]

[illegible]                                                          [illegible]
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Leu Trp Cys Ile Thr Ala Phe Thr Thr Ala Ala Ser Ala Tyr Ser Tyr
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Tyr His Tyr Tyr Arg Lys Thr Val Thr Val Ile Lys Asp
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<210> 24
<211> 1143
<212> DNA
<213> Homo sapiens

<220>
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<222> (12)..(1167)

<400> 24
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                        Met Glu Ala Leu Gly Lys Leu Lys Gln Thr
                          1               5                  10

gat gcc tat ccc aag acc ttg gag gac ttc cgg gtc aag acc tgc ggg      95
Asp Ala Tyr Pro Lys Thr Leu Glu Asp Phe Arg Val Lys Thr Cys Gly
                    15                  20                  25

ggc gcc act gtg acc atc gtc agt ggg ctc ctc atg ctg ctc ttc      143
Gly Ala Thr Val Thr Ile Val Ser Gly Leu Leu Met Leu Leu Phe
                30                  35                  40

ctg tcc gag ctg cag tat tac ctc acc cgc gag gtg cat cct gag ctc      191
Leu Ser Glu Leu Gln Tyr Tyr Leu Thr Arg Glu Val His Pro Glu Leu
            45                  50                  55

tac gtg gac aag tcg cgc ggc gtg gat gcc ttc gtc aag atc aac atc gac      239
Tyr Val Asp Lys Ser Arg Gly Asp Lys Leu Lys Ile Asn Ile Asp Val
        60                  65                  70

ctt ttc ccg cac atg ccc tgt gcc tac ctc tcc atc gac gcc atg gac      287
Leu Phe Pro His Met Pro Cys Ala Tyr Leu Ser Ile Asp Ala Met Asp
    75                  80                  85

                                                    335

                                                    383

                                                    431

                                                    479

                                                    527
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[illegible] tgt aac [illegible] [illegible] [illegible] gat gtg [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] 531
Cys Cys Asn Thr Cys Glu Asp Val Arg Glu Ala Tyr Arg Arg Arg Gly
155 160 165 170

[illegible] [illegible] ttc [illegible] aac [illegible] [illegible] act att [illegible] [illegible] [illegible] [illegible] cga [illegible] [illegible] 579
Trp Ala Phe Lys Asn [illegible] Asp Thr Ile Glu Gln Tyr Arg Arg Glu Gly
175 180 185

[illegible] [illegible] cag [illegible] [illegible] [illegible] [illegible] cag aag [illegible] [illegible] [illegible] tgc cag [illegible] [illegible] 627
Ile Ser Gln Lys Met Gln Glu Gln Lys Asn Glu Gly Cys Gln Val Tyr
190 195 200

[illegible] [illegible] ttg gaa [illegible] aat aag gtg [illegible] [illegible] [illegible] [illegible] cac ttt [illegible] [illegible] 675
Gly Phe Leu Glu Val Asn Lys Val Ala Gly Asn Phe His Phe Ala Pro
205 210 215

ggg aag agc ttc [illegible] cag [illegible] cat [illegible] [illegible] [illegible] [illegible] gac ttg cag [illegible] 723
Gly Lys Ser Phe Gln Gln Ser His Val His Val His Asp Leu Gln Ser
220 225 230

[illegible] ggc ctt gac [illegible] [illegible] aac atg acc [illegible] [illegible] [illegible] cag cac [illegible] [illegible] 771
Phe Gly Leu Asp Asn Ile Asn Met Thr His Tyr Ile Gln His Leu Ser
235 240 245 250

ttt ggg gag gac tat cca ggc att gtg aac ccc ctg gac cac acc aat 819
Phe Gly Glu Asp Tyr Pro Gly Ile Val Asn Pro Leu Asp His Thr Asn
255 260 265

[illegible] act gcg ccc caa [illegible] [illegible] atg atg [illegible] [illegible] [illegible] ttt gtg aag [illegible] 867
Val Thr Ala Pro Gln Ala Ser Met Met Phe Gln Tyr Phe Val Lys Val
270 275 280

[illegible] [illegible] act [illegible] [illegible] [illegible] aag gtg [illegible] [illegible] [illegible] [illegible] ctg agg [illegible] [illegible] 915
Val Pro Thr Val Tyr Met Lys Val Asp Gly Glu Val Leu Arg Thr Asn
285 290 295

[illegible] ttc tct gtg [illegible] [illegible] cat gag aag [illegible] [illegible] aat ggg ctg ttg [illegible] 963
Gln Phe Ser Val Thr Arg His Glu Lys Val Ala Asn Gly Leu Leu Gly
300 305 310

[illegible] 1011
Asp [illegible] Gly [illegible] [illegible] Gly Val Ile Val [illegible] Tyr [illegible] [illegible] [illegible] [illegible] Met

[illegible] 1059
Met Val Lys Leu Thr Glu Lys His Arg Ser Ile Thr His Phe Leu Thr
335 340 345

[illegible] 1107
Gly Val Tyr Ala Ile Ile Gly Gly Met Phe Thr Val Ala Gly Leu Ile

Leu Gly Lys Thr Thr
340

<210> 31
<211> 345
<212> PRT
<213> Homo sapiens

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Leu Glu Asp Phe Arg Val Lys Thr Cys Gly Gly Ala Thr Val Thr Ile
20 25 30

Val Ser Gly Leu Leu Met Leu Leu Leu Leu Leu Leu Ser Glu Leu Gln Tyr
35 40 45

Tyr Leu Thr Thr Glu Val His Pro Glu Leu Tyr Val Asn Lys Ser Arg
50 55 60

Gly Asp Lys Leu Lys Ile Asn Ile Asp Val Leu Phe Pro His Met Pro
65 70 75 80

Cys Ala Tyr Leu Ser Ile Asp Ala Met Asp Val Ala Gly Glu Gln Gln
85 90 95

Leu Asp Val Glu His Asn Leu Phe Lys Gln Arg Leu Asp Lys Asp Gly
100 105 110

Ile Pro Val Ser Ser Glu Ala Glu Arg His Glu Leu Gly Lys Val Glu
115 120 125

Val Thr Val Phe Asp Pro Asp Ser Leu Asp Pro Asp Arg Cys Glu Ser
130 135 140

Tyr Tyr Gly Ala Ile Ala Ile Arg Leu Lys Tyr Tyr Ala Ile Tyr Lys
145 150 155 160

Arg Val Arg Glu Ala Tyr Arg Arg Arg Lys Trp Ala Leu Ile Lys
165 170 175

Asp Thr Ile Glu Gln Cys Arg Arg Arg Gly Ile Ser His Tyr Met Thr
180 185 190

Leu Lys Lys Asn Ala Gly Tyr Leu Thr Tyr Gly Ile Leu Val Asn
195 200 205

```
Ser His Val His Val His Asp Leu Gln Ser Phe Gly Leu Asp Asn Ile
225                 230                 235                 240

Asn Met Thr His Tyr Ile Gln His Leu Ser Phe Gly Glu Asp Tyr Pro
                245                 250                 255

Gly Ile Val Asn Pro Leu Asp His Thr Asn Val Thr Ala Pro Asn Ala
            260                 265                 270

Ser Met Met Phe Gln Tyr Phe Val Lys Val Val Pro Thr Val Tyr Met
        275                 280                 285

Lys Val Asp Gly Glu Val Leu Arg Thr Asn Gln Phe Ser Val Thr Arg
    290                 295                 300

His Glu Lys Val Ala Asn Gly Leu Leu Gly Arg Gln Gly Leu Pro Gly
305                 310                 315                 320

Val Phe Val Leu Tyr Glu Leu Ser Pro Met Met Val Lys Leu Thr His
                325                 330                 335

Lys His Arg Ser Phe Thr His Phe Leu Thr Gly Val Cys Ala Ile Ile
            340                 345                 350

Gly Gly Met Phe Thr Val Ala Gly Leu Ile Asp Ser Leu Ile Tyr His
        355                 360                 365

Ser Ala Arg Ala Ile Gln Lys Lys Ile Asp Leu Gly Lys Thr Thr
    370                 375                 380
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<212> DNA
<213> Homo sapiens

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<222> (19)..(877)

<400> 31
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Pro Ser Phe Val Ala Ala Val Ile Thr Ile Thr Phe Asn Ile Leu Tyr
                                                                   300

                                                                   360
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45 50 55 60

[illegible] 301
Leu Leu Leu Asn Phe Leu Arg Ser His Cys Phe Thr Gln Ala Met Leu
65 70 75

[illegible] 349
Ser Gln Pro Arg Met Glu Ser Leu Asp Thr Pro Ala Ala Tyr Ser Leu
80 85 90

[illegible] 397
Gly Leu Ala Leu Leu Gly Leu Gly Val Val Leu Val Leu Ser Ser Phe
95 100 105

ttt gca ctg ggg ttc gct gga act ttc cta ggt gat tac ttc ggg atc 445
Phe Ala Leu Gly Phe Ala Gly Thr Ile Leu Gly Asp Tyr Phe Gly Ile
110 115 120

[illegible] 493
Leu Lys Glu Ala Arg Val Thr Val Phe Pro Phe Asn Ile Leu Asp Asn
125 130 135 140

[illegible] 541
Pro Met Tyr Trp Gly Ser Thr Ala Asn Tyr Leu Gly Trp Ala Ile Met
145 150 155

cac gct agc ccc acg ggc ctg ctc ctg acg gtg ctg gtg gct ctc acc 589
His Ala Ser Pro Thr Gly Leu Leu Leu Thr Val Leu Val Ala Leu Thr
160 165 170

tac ata gtg gct ctc cta tac gaa gag ccc ttc acc gct gag atc tac 637
Tyr Ile Val Ala Leu Leu Tyr Glu Glu Pro Phe Thr Ala Glu Ile Tyr
175 180 185

[illegible] 690
Arg Gln Lys Ala Ser Gly Ser His Lys Arg Ser
190 195

[illegible] 750

[illegible] 810

[illegible]

[illegible]

[illegible]

Ala Arg Trp Val His Lys Thr Arg Lys Leu Ser Arg Ala Ile Gly Ser
35 40 45

Ile Tyr Leu Ala Tyr Tyr Ser Leu Ser Val Thr Ile Leu Leu Ile Asn
50 55 60

Phe Leu Arg Ser His Cys Phe Thr Val Ala Met Leu Ser Pro Ile Ile Arg
65 70 75 80

Met Glu Ser Leu Asp Thr Ile Ala Ala Tyr Ser Leu Gly Leu Ala Leu
85 90 95

Leu Gly Leu Gly Val Val Leu Val Leu Ser Ser Phe Phe Ala Leu Gly
100 105 110

Phe Ala Gly Thr Phe Leu Gly Asp Tyr Ile Gly Ile Leu Lys Glu Ala
115 120 125

Arg Val Thr Val Phe Pro Phe Asn Ile Leu Asp Asn Pro Met Tyr Trp
130 135 140

Gly Ser Thr Ala Asn Tyr Leu Gly Trp Ala Ile Met His Ala Ser Pro
145 150 155 160

Thr Gly Leu Leu Leu Thr Val Leu Val Ala Leu Thr Tyr Ile Val Ala
165 170 175

Leu Leu Tyr Glu Glu Pro Phe Thr Ala Glu Ile Tyr Arg Glu Lys Ala
180 185 190

Ser Gly Ser His Lys Arg Ser
195

<210> 33
<211> 903
<212> DNA
<213> Homo sapiens

[illegible]

[illegible]

Met Ala Pro His Gly Pro Gly Ser Leu Thr Thr Leu Val Pr

[illegible]

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Lys Val Ala Phe Tyr Cys Lys Thr Thr Arg Glu Leu Met Leu His Ala
                 35                  40                  45

ttt tgt tgc ctg aat cag aaa ata att ata ttg ggt ctt gat ctg cta   192
Phe Cys Cys Leu Asn Gln Lys Ile Ile Ile Leu Gly Leu Asp Leu Leu
             50                  55                  60

aat tgt tct ctg gaa gat cca ggt ata aat ttt cat cag gca cat act a t   240
Asn Cys Ser Leu Glu Asp Pro Gly Ile Asn Phe His Gln Ala His Thr
         65                  70                  75

act gtc atc ata gac ctg caa gca aat cct ctc aaa ggt gac ttg gct a t   288
Thr Val Ile Ile Asp Leu Gln Ala Asn Pro Leu Lys Gly Asp Leu Ala
     80                  85                  90                  95

aac acc ttc cgt ggt ttt act caa ctg cag act ctg ata ctg cca caa   336
Asn Thr Phe Arg Gly Phe Thr Gln Leu Gln Thr Leu Ile Leu Pro Gln
                100                 105                 110

cat gtc aac tgt cct gga ggt att aat gct tgg aat act atc acc tct   384
His Val Asn Cys Pro Gly Gly Ile Asn Ala Trp Asn Thr Ile Thr Ser
            115                 120                 125

tat ata gac aac caa atc tgt caa ggg caa aag aac ctt tgc aat aac   432
Tyr Ile Asp Asn Gln Ile Cys Gln Gly Gln Lys Asn Leu Cys Asn Asn
        130                 135                 140

act ggg gac cca gaa atg tgt ttt aat gga tct tgt gta cct gtt   480
Thr Gly Asp Pro Glu Met Cys Phe Asn Gly Ser Cys Val Pro Asp
    145                 150                 155

ggt cca ggt ctt ttg cag tgt gtt tgt gct gat ggt ttc cat gga tat   528
Gly Pro Gly Leu Leu Gln Cys Val Cys Ala Asp Gly Phe His Gly Tyr
160                 165                 170                 175

aag tgt atg cgc caa ggt tct ttt tca ctg ctt atg ttc ttc ggg att   576
Lys Cys Met Arg Gln Gly Ser Phe Ser Leu Leu Met Phe Phe Gly Ile
                180                 185                 190

t t ttg gct tta tta tta t t tgg ctt tgg gct tta tta   624
  Leu Ala Leu Leu Leu   Trp Leu Trp Ala Leu Leu
            195                 200

aga aga aaa gct aaa tca act cct gtt aat aaa gct gtt tat caa caa   672
Arg Arg Lys Ala Lys Ser Thr Pro Val Asn Lys Ala Val Tyr Gln Gln
        210                 215                 220

ctt aat cac tgt aaa aga aat aga gat gtt tct caa gtt tct ttg gaa   720
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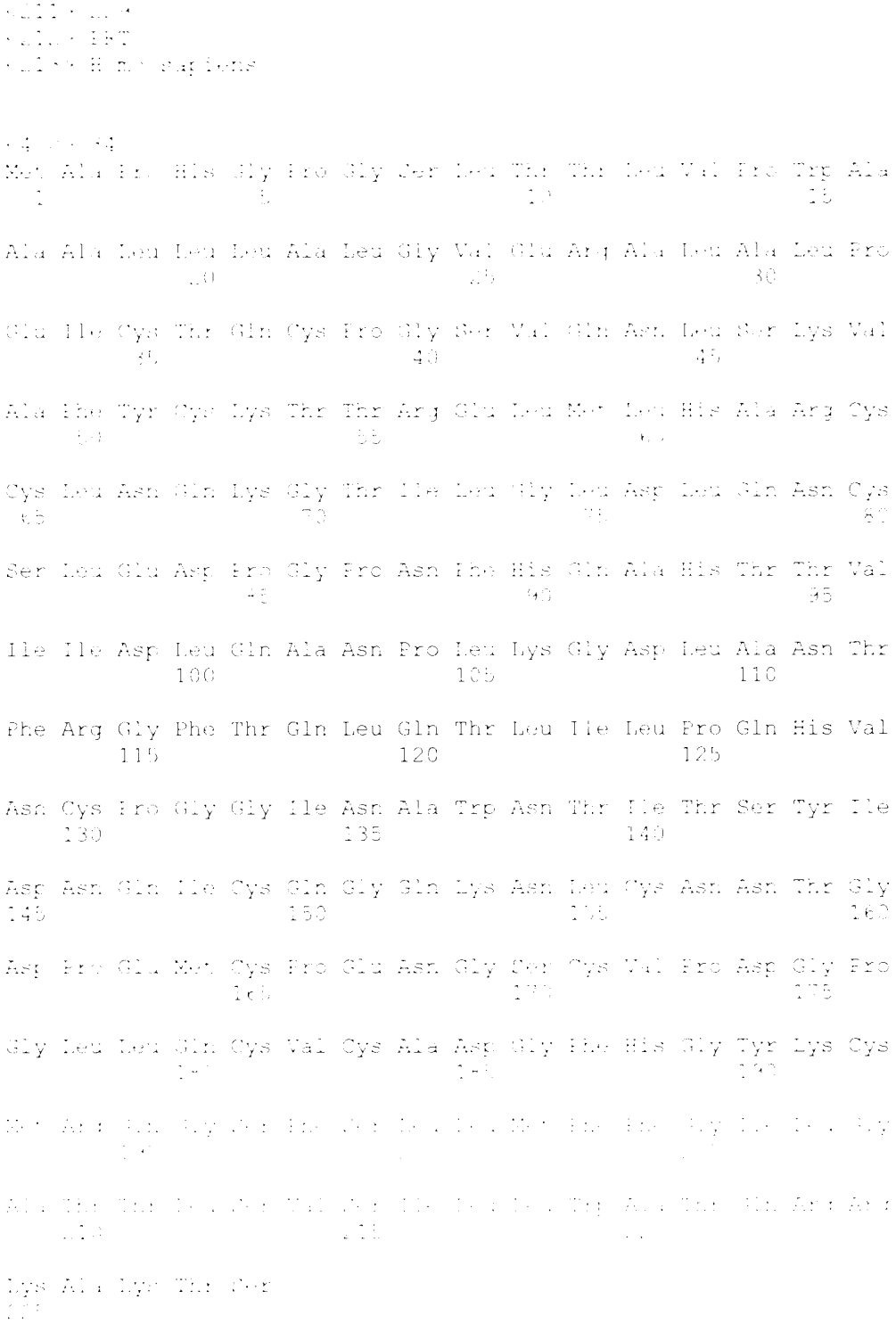

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<400> 35

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                                                                  Met Asp Ile Asp Gly Arg                 47
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Met Lys Ser Leu Leu Thr Thr Val Gly Leu Leu Leu Ile Thr Arg Gly Thr      95
Leu Cys Leu Leu Thr Ile Val Gly Leu Leu Ile Thr Thr Arg Gly Thr
            10                  15                  20

Thr Leu Lys Asp Thr Thr Asn Asn Asn Asn Ala Asp Asn Thr Ile Met     143
        25                  30                  35

Asp Ile Gln Val Pro Thr Arg Ala Pro Asp Ala Val Tyr Thr Glu Leu     191
    40                  45                  50

Gln Pro Thr Ser Pro Thr Pro Thr Trp Pro Ala Asp Glu Thr Pro Gln     239
55                  60                  65                  70

Pro Gln Thr Gln Thr Gln Gln Leu Glu Gly Thr Asp Gly Pro Leu Val     287
                75                  80                  85

Thr Asp Pro Glu Thr His Lys Ser Thr Lys Ala Ala His Pro Thr Asp     335
            90                  95                 100

Asp Thr Thr Thr Leu Ser Glu Arg Pro Ser Pro Ser Thr Asp Val Gln     383
        105                 110                 115

Thr Asp Pro Gln Thr Leu Lys Pro Ser Gly Phe His Glu Asp Asp Pro     431
    120                 125                 130

Ile Ile Tyr Asp Phe His Thr Leu Arg Lys Arg Leu Leu Val Ala      479
135                 140                 145

Ala Val Leu Phe Ile Thr Gly Ile Ile Leu Leu Thr Val Gly Lys Tyr     527
                150                 155                 160

Arg Thr Leu Ile Asn His Tyr Arg                                     551
            165                 170
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[illegible]

[illegible]

[illegible]

<211> 46
<212> PRT
<213> Homo sapiens

<400> 46
Met Ser Pro Ser Gly Arg Leu Cys Leu Leu Thr Ile Val Gly Leu Ile
1 5 10 15

Leu Pro Thr Arg Gly Gln Thr Leu Lys Asp Thr Thr Ser Ser Ser Ser
20 25 30

Ala Asp Ser Thr Ile Met Asp Ile Gln Val Pro Thr Arg Ala Pro Asp
35 40 45

Ala Val Tyr Thr Glu Leu Gln Pro Thr Ser Pro Thr Pro Thr Trp Pro
50 55 60

Ala Asp Glu Thr Pro Gln Pro Gln Thr Gln Thr Gln Gln Leu Glu Gly
65 70 75 80

Thr Asp Gly Pro Leu Val Thr Asp Pro Glu Thr His Lys Ser Thr Lys
85 90 95

Ala Ala His Pro Thr Asp Asp Thr Thr Thr Leu Ser Glu Arg Pro Ser
100 105 110

Pro Ser Thr Asp Val Gln Thr Asp Pro Gln Thr Leu Lys Pro Ser Gly
115 120 125

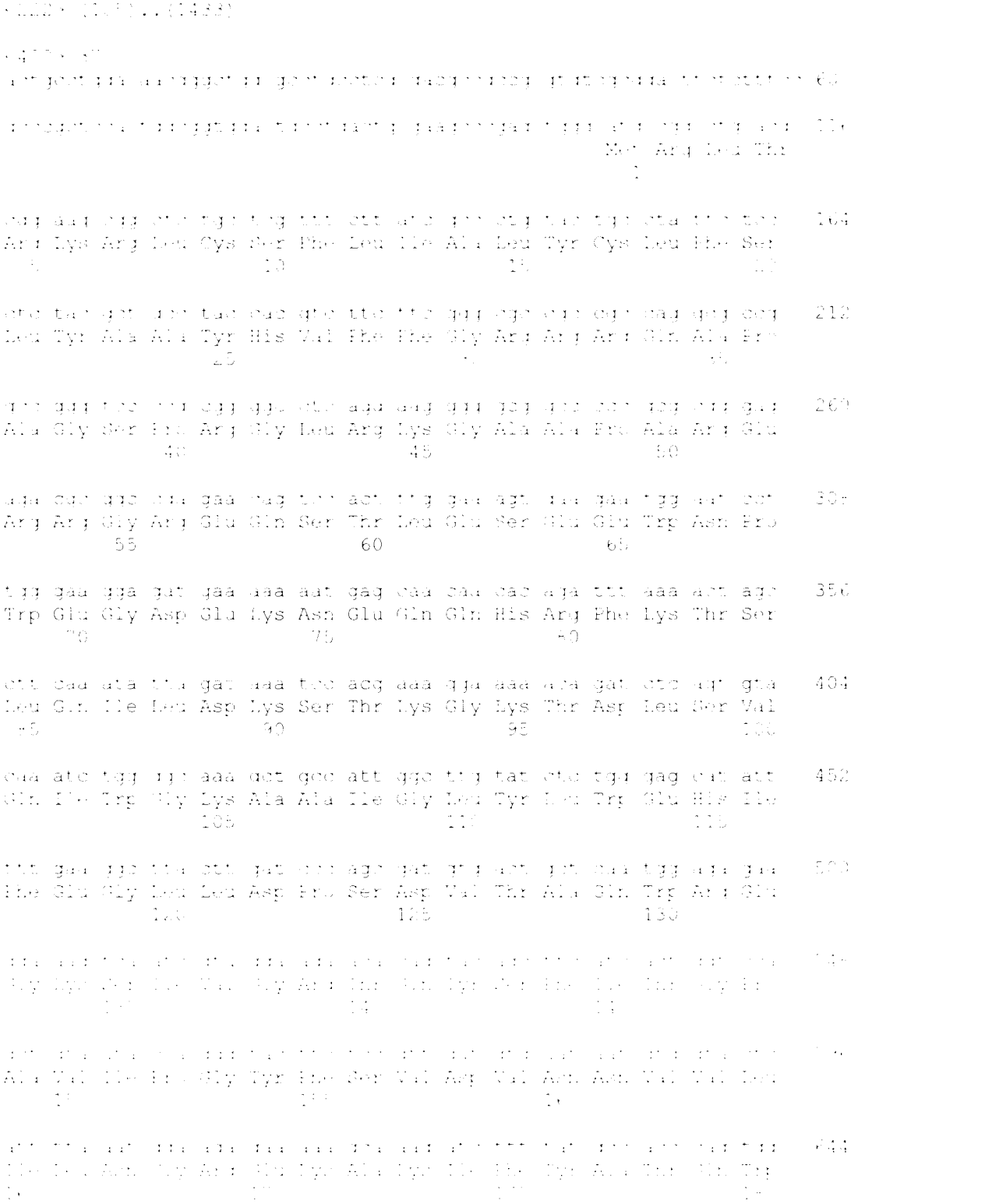
Phe His Glu Asp Asp Pro Phe Phe Tyr Asp Glu His Thr Leu Arg Lys
130 135 140

Arg [illegible]
145 150

[illegible]

Tyr Arg

[illegible]



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gct gtt gtt ttg ctt gga aat gaa cat tgt gat aat gat tgg gta aac      744
Ala Val Val Leu Leu Gly Asn Glu His Cys Asp Asn Asp Trp Val Asn
                215                 220                 225

cca ttc ttt aaa aga aat aac gga ttt gat gtt gaa ctt ttc ata ata      792
Pro Phe Leu Lys Arg Asn Asn Gly Phe Asp Val Glu Leu Phe Ile Ile
            230                 235                 240

tat gac agt cct tgg att aac gat gac gtt gat gtt ttt caa tgg ccg      840
Tyr Asp Ser Pro Trp Ile Asn Asp Val Asp Val Phe Gln Trp Pro
        245                 250                 255

gga gta gca act tat agg aat ttt ccg gat gaa gca agt tgg gta aaa      888
Gly Val Ala Thr Tyr Arg Asn Phe Pro Asp Glu Ala Ser Trp Val Lys
    260                 265                 270

atg ttg cat gat gaa agg ccg tat tta tgt aat ttc ctt ggg acg att      936
Met Leu His Asp Glu Arg Pro Tyr Leu Cys Asn Phe Leu Gly Thr Ile
275                 280                 285

tat gaa aat agc tca tct aga cag gca tta atg aac att tta aaa aaa      984
Tyr Glu Asn Ser Ser Arg Gln Ala Leu Met Asn Ile Leu Lys Lys Asp
290                 295                 300

ggg aac gat aag ctt tgt tgg gtt tca gca aga gaa cac tgg caa cct     1032
Gly Asn Asp Lys Leu Cys Trp Val Ser Ala Arg Glu His Trp Gln Pro
305                 310                 315

cag gaa aca aat gaa gtt agt tta aag aat tac caa gat gca tta ttg     1080
Gln Glu Thr Asn Glu Ser Leu Lys Asn Tyr Gln Asp Ala Leu Leu Gln
320                 325                 330

agt gat tta aca ttg tgc cct gtc ggg gta aac aca gaa tgt tat cga     1128
Ser Asp Leu Thr Leu Cys Pro Val Gly Val Asn Thr Glu Cys Tyr Arg
335                 340                 345

att tat gaa gca ttc tat tca tat ggc tcc att cct gtg ttg gaa gac     1176
Ile Tyr Glu Ala Phe Tyr Ser Tyr Gly Ser Ile Pro Val Leu Glu Asp
350                 355                 360

atg aca ttt gtc gat ttt ctt aat aca tta aat gtt gat gat aat gtt     1224
Met Thr Phe Val Asp Phe Leu Asn Thr Leu Asn Val Asp Asp Asn Val
365                 370                 375

ttt aag aaa ttt ctg ttt gct gtt tta aat aaa gaa aaa ttt aaa ttt     1272
Phe Lys Lys Phe Leu Phe Ala Val Leu Asn Lys Glu Lys Phe Lys Phe
380                 385                 390

ttg ttt tga tttttttttt ttttttttta ttttttttta ttttttttta ttttttttta     1324
Leu Phe
395
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Phe Lys Thr Glu Leu Lys Met Lys Ile Thr Asn Ile Leu Asn Ser Ser
420 425 430

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Phe Leu Met Asn Asn Lys Ser
435

<210> 17
<211> 443
<212> PRT
<213> Homo sapiens

<400> 17
Met Arg Leu Thr Arg Lys Arg Leu Cys Ser Phe Leu Ile Ala Leu Tyr
1 5 10 15

Cys Leu Phe Ser Leu Tyr Ala Ala Tyr His Val Thr Thr Gly Arg Arg
20 25 30

Arg Gln Ala Pro Ala Gly Ser Pro Arg Gly Leu Arg Lys Gly Ala Ala
35 40 45

Pro Ala Arg Glu Arg Arg Gly Arg Glu Gln Ser Thr Leu Glu Ser Glu
50 55 60

Glu Trp Asn Pro Trp Glu Gly Asp Glu Lys Asn Glu Gln Gln His Arg
65 70 75 80

Phe Lys Thr Ser Leu Gln Ile Leu Asp Lys Ser Thr Lys Gly Lys Thr
85 90 95

Asp Leu Ser Val Gln Ile Trp Gly Lys Ala Ala Ile Gly Leu Tyr Leu
100 105 110

Trp Glu His Ile Phe Glu Gly Leu Leu Asp Pro Ser Asp Val Thr Ala
115 120 125

Gln Trp Arg Glu Gly Lys Ser Ile Val Gly Arg Thr Gln Tyr Ser Phe
130 135 140

[illegible]

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...  ...  ...  ...  ...  ...  ...  ...  ...  ...  ...  ...  ...  ...  ...
...  Trp  Pro  Leu  Gly  Val  Ala  Thr  Tyr  Arg  Asn  Ile  Pro  Val  Val  Glu
                   140                       250                       265

Ala  Ser  Trp  Ser  Met  Leu  His  Asp  Glu  Arg  Pro  Tyr  Leu  Lys  Asn  Pro
               260                       280                       295

Leu  Gly  Thr  Ile  Tyr  Glu  Asn  Ser  Ser  Arg  Gln  Ala  Leu  Met  Asn  Ile
          275                       290                       305

Leu  Lys  Lys  Asp  Gly  Asn  Asp  Lys  Leu  Cys  Trp  Val  Ser  Ala  Arg  Glu
     310                       325                       340

His  Trp  Gln  Pro  Gln  Glu  Thr  Asn  Glu  Ser  Leu  Lys  Asn  Tyr  Gln  Asp
345                       360                       375

Ala  Leu  Leu  Gln  Ser  Asp  Leu  Thr  Leu  Cys  Pro  Val  Gly  Val  Asn  Thr
               380                       395                       410

Glu  Cys  Tyr  Arg  Ile  Tyr  Glu  Ala  Cys  Ser  Tyr  Gly  Ser  Ile  Pro  Val
          415                       430                       445

Val  Glu  Asp  Val  Met  Thr  Ala  Gly  Asn  Cys  Gly  Asn  Thr  Ser  Val  His
     450                       465                       480

His  Gly  Ala  Pro  Leu  Gln  Leu  Leu  Lys  Ser  Met  Gly  Ala  Pro  Phe  Ile
485                       500                       515

Phe  Ile  Lys  Asn  Trp  Lys  Glu  Leu  Pro  Ala  Val  Leu  Glu  Lys  Glu  Lys
               520                       535                       550

Thr  Ile  Ile  Leu  Gln  Glu  Lys  Ile  Glu  Arg  Arg  Lys  Met  Leu  Leu  Gln
          555                       570                       585

Trp  Tyr  Gln  His  Ile  Lys  Thr  Glu  Leu  Lys  Met  Lys  Phe  Thr  Asn  Ile
     590                       605                       620

Leu  Glu  Ser  Ser  Phe  Leu  Met  Asn  Asn  Lys  Ser
625                       640
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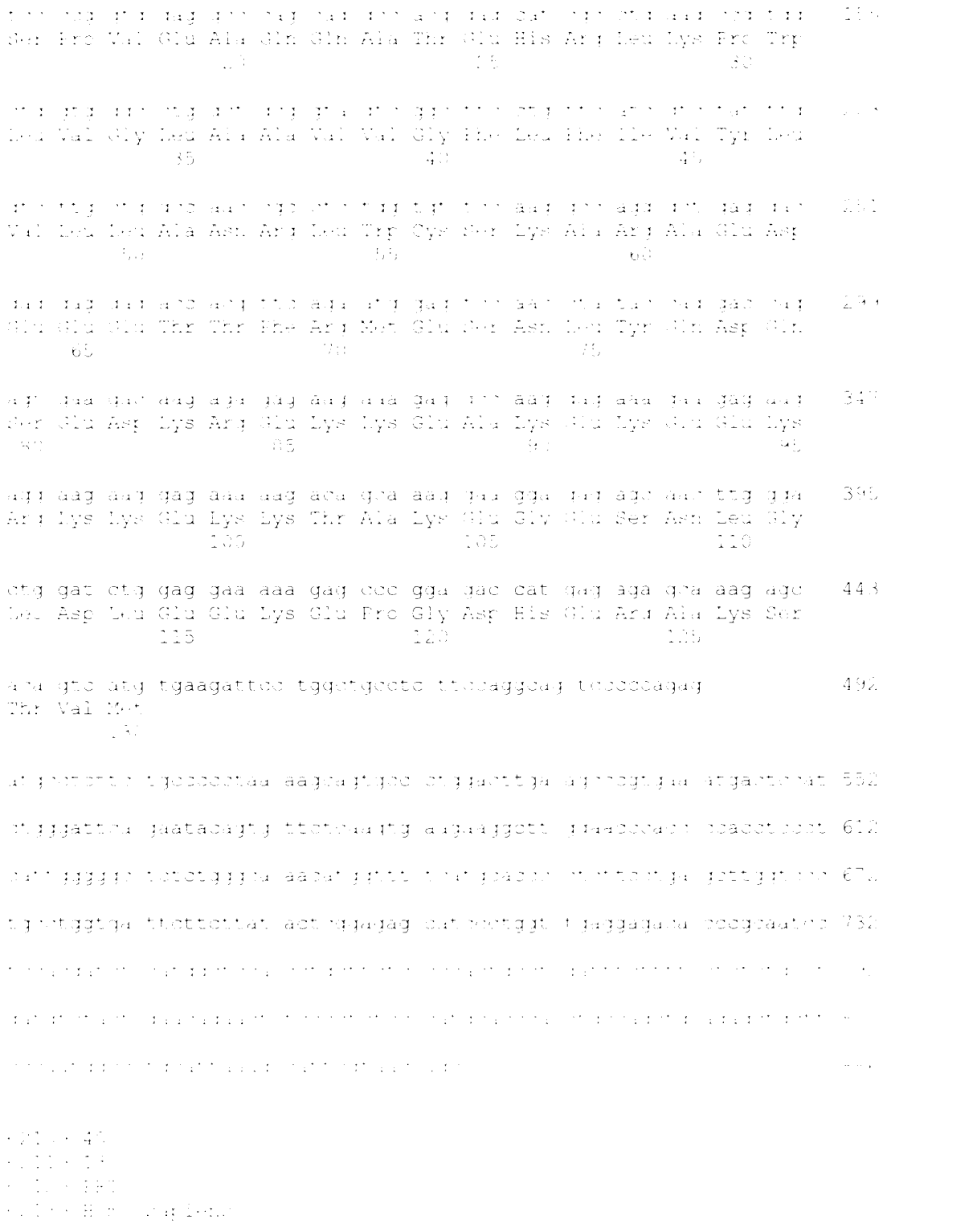

Pro Val Ala Ala Gln Gln Ala Thr Glu His Arg Leu Lys Pro Trp Leu
Val Gly Leu Ala Ala Val Val Gly Phe Leu Leu Ile Val Tyr Leu Val
Leu Leu Ala Asn Arg Leu Trp Tyr Ser Lys Ala Arg Ala Glu Asp Lys
Glu Gly Thr Thr Phe Arg Met Gln Ser Asn Leu Tyr Gln Asp Gln Ser
Glu Asp Lys Arg Glu Lys Lys Glu Ala Lys Glu Lys Glu Glu Lys Arg
Lys Lys Pro Lys Lys Thr Ala Lys Glu Gly Glu Ser Asn Leu Gly Leu
Asp Leu Leu Glu Lys Glu Pro Gly Asp His Glu Arg Ala Lys Ser Thr
Val Met
130

<210> 41
<211> 14
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Chimeric cDNA-RNA oligonucleotide

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gggaaatcga ttga 14

<210> 42
<211> 130
<212> PRT
<213> Homo sapiens

<400> 42
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Arg Ala His Thr Leu Leu Tyr Phe Ser Tyr Ser Arg Ala Ser Ser Asn
Thr Ala Tyr Leu Thr Ile Val Tyr Ala Leu Asn Glu Glu His Tyr

<400> 43
Met Ser Met Ser Leu Glu Ile Thr Gly Thr Ser Leu Ala Val Leu Gly
1 5 10 15

Trp Leu Cys Thr Ile Val Cys Cys Ala Leu Pro Met Trp Arg Val Ser
20 25 30

Ala Phe Ile Gly Ser Ser Ile Ile Thr Ala Gln Ile Thr Trp Glu Gly
35 40 45

Leu Trp Met Asn Cys Val Gln Ser Thr Gly Gln Met Gln Cys Lys Met
50 55 60

Tyr Asp Ser Leu Leu Ala Leu Pro Gln Asp Leu Gln Ala Ala Arg Ala
65 70 75 80

Leu Ile Val Val Ser Ile Leu Leu Ala Ala Phe Gly Leu Leu Val Ala
85 90 95

Leu Val Gly Ala Gln Cys Thr Asn Cys Val Gln Asp Glu Thr Ala Lys
100 105 110

Ala Lys Ile Thr Ile Val Ala Gly Val Leu Phe Leu Leu Ala Ala Val
115 120 125

Leu Thr Leu Val Pro Val Ser Trp Ser Ala Asn Thr Ile Ile Arg Asp
130 135 140

Ile Tyr Asn Ile Leu Val Ile Ser Leu Ala Leu Tyr Asn Leu Met Leu Thr
145 150 155 160

Gly Leu Tyr Val Gly Trp Ala Ala Ala Ala Ala Leu Gln Leu Leu Gly Gly
165 170 175

Ala Leu Leu Tyr Tyr Ser Tyr Ser Ile Ile Arg Ser Tyr Ala Ile Ile
180 185 190

Gly Thr Ala Tyr Asp Arg Lys Thr Thr [illegible] Glu Arg Pro Gly Ala Arg
210 215 220

Thr Pro His His His His Tyr Gln Pro Met Ser Tyr Pro Thr
225 230 235

<211> 44
<212> PRT
<213> Caenorhabditis elegans

<400> 44
Met Cys Asn Phe Ser Tyr Phe Gln Leu Gln Met Gly Ile Leu Ile Pro
1 5 10 15

Leu Val Ser Val Ser Ala Phe Trp Ala Ile Ile Gly Pro Gly Gly Pro
20 25 30

Trp Ile Val Pro Lys Gly Pro Asn Arg Gly Ile Ile Gln Leu Met Ile
35 40 45

Ile Met Thr Ala Val Cys Cys Trp Met Phe Trp Ile Met Val Phe Leu
50 55 60

His Gln Leu Asn Pro Leu Ile Gly Pro Gln Ile Asn Val Lys Thr Ile
65 70 75 80

Arg Trp Ile Ser Glu Lys Trp Gly Asp Ala Pro Asn Val Ile Asn Asn
85 90 95

<210> 45
<211> 246
<212> PRT
<213> Caenorhabditis elegans

<400> 45
Met Ile Val Thr Ser Met Phe Arg Gly Ile Ala Cys Arg Cys Glu Leu
1 5 10 15

[illegible]

[illegible]

Gly Lys Tyr Lys Val Ala Thr Ile [illegible] Asn Ala Ile Tyr Thr Ala Arg
50 55 60

[illegible]

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                1               5                  10                  15

Ser Val Leu Asp Pro Val Ala Asp Lys Leu Leu Ile Ser Thr Met Ile
            115                 120                 125

Ile Thr Met Thr Tyr Ala Gly Leu Ile Pro Leu Ile Leu Leu Thr Ser Val
        130                 135                 140

Val Ile Leu Arg Asp Ile Cys Leu Ile Gly Gly Gly Phe Tyr Lys Arg
145                 150                 155                 160

Tyr Gln Val Met Ser Pro Pro Tyr Ser Leu Ser Arg Phe Phe Asn Pro
                165                 170                 175

Gln Val Ser Ser Met Gln Val Val Pro Thr Met Met Ser Lys Ile Asn
            180                 185                 190

Thr Val Leu Gln Ile Thr Leu Val Ala Leu Ser Leu Gln Ser Ser Pro Val
        195                 200                 205

Phe Asp Phe Ser Thr Gly Ala Asn Asp Val Ile Val Gly Leu Gly Cys
    210                 215                 220

Ile Thr Gly Phe Thr Thr Ile Tyr Ser Gly Leu Gln Tyr Ala Ser Gly
225                 230                 235                 240

Lys Ala Ile Lys Lys Ile
                245
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<210> 46
<211> 346
<212> PRT
<213> Caenorhabditis elegans

<400> 46

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Met Ser Leu Leu Trp Ser Leu Lys His Phe Asp Ala Tyr Arg Lys Pro
  1               5                  10                  15

Met Asp Asp Phe Arg Val Lys Thr Leu Ser Gly Gly Leu Val Thr Leu
            20                  25                  30

Ile Ala Ile Ile Ala Ile Thr Leu Leu Ile Ile Thr Ile Ile Pro Ile Thr Lys Leu
        35                  40                  45

Ile Tyr Ile Ile Ile Val Ile Ile Thr Val Asp Ile Asp Thr Thr Asp
    50                  55                  60

Ser Asp Glu Arg Val His Ile Val Glu Phe Asp Ile Thr Ile Thr Lys Leu
65                  70                  75                  80

Ile Tyr Asn Ile Ile Thr Val Asp Val Met Asp Val Ser Ser Val Ala
                85                  90                  95
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Gly Arg Asn Ile Pro Ser Ser Ala Gln Lys Ile Ser Ile Asn Ala Asn
110 115

Lys Thr Ser Val Glu Thr Thr Asp Val Ile Gln Ser Val Lys Cys Gly
130 135 140

Ser Cys Tyr Gly Ala Ala Ala Asp Gly Ile Cys Cys Asn Thr Cys Arg
145 150 155 160

Asp Val Lys Ser Ala Tyr Ala Val Lys Gly Trp Val Asn Ile Glu
165 170 175

Glu Val Glu Gln Cys Lys Asn Asp Lys Trp Val Lys Glu Thr Asn Glu
180 185 190

His Lys Asn Glu Gly Cys Arg Val Tyr Gly Thr Val Lys Val Ala Lys
195 200 205

Val Ala Gly Asn Phe His Leu Ala Pro Gly Asp Pro His Gln Ala Met
210 215 220

Arg Ser His Val His Asp Leu His Asn Leu Asp Pro Val Lys Phe Asp
225 230 235 240

Ala Ser His Thr Val Asn His Val Ser Phe Gly Lys Ser Phe Pro Gly
245 250 255

Lys Asn Tyr Pro Leu Asp Gly Lys Val Asn Thr Asp Asn Arg Gly Gly
260 265 270

Ile Met Tyr Gln Tyr Tyr Val Lys Val Val Pro Thr Arg Tyr Asp Tyr
275 280 285

Leu Asp Gly Arg Val Asp Gln Ser His Gln Phe Ser Val Thr Thr His
290 295 300

Lys Lys Asp Leu Gly Phe Arg Gln Ser Gly Leu Pro Gly Phe Phe Leu
305 310 315 320

Gln Tyr Glu Phe Ser Pro Leu Met Val Gln Tyr Glu Glu Phe Arg Gln
325 330 335

Ile Ala Ser Ile Leu Val Ser Ile Ile Tyr Ala Ile Val Gly Gly
340 345 350

Met Ala Ala Ile Val Asn Ile Ile Lys His Ile Asp
355 360 365

Tyr Met Lys Pro Arg Ile Ala Gly Gly Lys Leu Thr
370 375 380

Ser Trp Leu Leu Gly Tyr Val Arg Pro Thr Gln Ile Ser Ile Val Ala
1 5 10 15

Ala Val Leu Thr Ile Val Phe Asn Ile Leu Phe Trp Asn Val Val Ala
20 25 30

Arg Trp Asn Gln Arg Thr Arg Lys Leu Ser Arg Ala Phe Gly Ser Pro
35 40 45

Tyr Leu Ala Cys Tyr Ser Leu Gly Ser Ile Ile Leu Leu Leu Asn Ile
50 55 60

Leu Arg Ser His Cys Phe Thr Gln Ala Met Met Ser Gln Pro Lys Met
65 70 75 80

Glu Gly Leu Asp Ser His Thr Ile Tyr Phe Leu Gly Leu Ala Leu Leu
85 90 95

Gly Trp Gly Leu Val Phe Val Leu Ser Ser Phe Tyr Ala Leu Gly Phe
100 105 110

Thr Gly Thr Phe Leu Gly Asp Tyr Phe Gly Ile Leu Lys Glu Ser Arg
115 120 125

Val Thr Thr Phe Pro Phe Ser Val Leu Asp Asn Pro Met Tyr Trp Gly
130 135 140

Ser Thr Ala Asn Tyr Leu Gly Trp Ala Leu Met His Ala Ser Pro Thr
145 150 155 160

Gly Leu Leu Leu Thr Val Leu Val Ala Leu Val Tyr Val Val Ala Leu
165 170 175

Leu Phe Glu Gln Pro Phe Thr Ala Glu Ile Tyr Arg Arg Lys Ala Thr
180 185 190

Arg Leu His Lys Arg Ser
195

Met Ser Leu Ser Ser Arg Leu Tyr Leu Leu Thr Ile Val Ala Leu Ile
1 5 10 15

Leu Ile Ala Arg Gly Val Thr Ile Tyr Lys Ile Ile Leu Ala Ile Ile

Ala Ala Thr Gly Ser Val Thr Ala Ala Gln Thr Val Thr Val Gln Leu
65 70 75 80

Thr Lys Met Ala Thr Ser Asn Pro Val Ser Asp Ile Gly Pro His Thr
85 90 95

Ser Ser Lys Lys Gly Thr Pro Ala Val Ser Arg Ile Gln Pro Leu Ser
100 105 110

Pro Ser Lys Asn Phe Met Pro Pro Ser Tyr Ile Gln His Pro Leu Asp
115 120 125

Ser Asn Glu Asn Asn Pro Phe Tyr Tyr Asp Asp Thr Thr Leu Arg Lys
130 135 140

Arg Gly Leu Leu Val Ala Ala Val Leu Phe Ile Thr Gly Ile Ile Ile
145 150 155 160

Leu Thr Ser Gly Lys Cys Arg Gln Leu Ser Gln Phe Cys Leu Asn Arg
165 170 175

His Arg